In the Claims

Please amend claims 11-14 as follows:

1. (original)   A method of modeling a directed evolution protocol comprising:

applying equilibrium thermodynamics to a plurality of sequences to determine statistics of

hybridization; and

parameterizing an assembly algorithm using the statistics of hybridization.

2. (original)   The method of claim 1 further comprising applying the assembly algorithm to

reassemble a plurality of sequences.

3. (original)   The method of claim 2 further comprising determining crossover allocation in the

plurality of reassembled sequences.

4. (original)   The method of claim 3 wherein the step of determining crossover allocation

includes estimating a fraction of the plurality of reassembled sequences containing a number of

crossovers.

5. (original)   The method of claim 3 wherein the step of determining crossover allocation

includes estimating a probability that a given nucleotide position in one of the plurality of

reassembled sequences is a site of a crossover event.

6. (original)   The method of claim 1 wherein the directed evolution protocol is DNA shuffling.

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7. (original)   The method of claim 1 wherein the directed evolution protocol is SCRATCHY.

8. (original)   The method of claim 1 further comprising identifying a minimum number of required silent mutations to meet a DNA recombination objective.

9. (original)   The method of claim 1 wherein the step of applying equilibrium thermodynamics to determine statistics of hybridization includes:

modeling annealing events during reassembly as a network of reactions;

determining a predicted fraction of fragments that will anneal at a given temperature;

determining a predicted distribution of annealing for overlap lengths; and

determining a portion of annealing events predicted to involve mismatches.

10. (original)   The method of claim 1 wherein the assembly algorithm excludes silent crossovers.

11. (currently amended)   An A method of providing an isolated nucleic acid molecule comprising:

providing a nucleotide sequence having an amino acid sequence;

the nucleotide sequence isolated at least in part through a directed evolution experiment; and

the directed evolution experiment selected at least in part by applying equilibrium

thermodynamics to a plurality of sequences to determine statistics of hybridization and

parameterizing an assembly algorithm using the statistics of hybridization.

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12. (currently amended)   ~~A~~ The method of claim 11 wherein a vector ~~comprising~~ comprises
the nucleic acid molecule ~~of claim 11~~.

13. (currently amended)   ~~A~~ The method of claim 12 wherein a host cell ~~containing~~ contains
the vector ~~of claim 12~~.

14. (currently amended)   ~~A~~ The method of claim 11 wherein the nucleotide sequence
encodes a protein, ~~encoded by the nucleic acid sequence of claim 11~~.

15. (original)   A system for modeling a directed evolution protocol comprising:

a plurality of sequences; and

an article of software for determining statistics of hybridization of the plurality of sequences to

   parameterize an assembly algorithm by applying equilibrium thermodynamics to the plurality

   of sequences.

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